

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/836,544 B  
Source: IFW/6  
Date Processed by STIC: 7-26-05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 01/26/2005

PATENT APPLICATION: US/09/836,544B

TIME: 14:35:01

Input Set : A:\11-881.app

Output Set: N:\CRF4\01262005\I836544B.raw

(pg. 6)

3 <110> APPLICANT: Brian Seed  
 4 Janet Allen  
 5 Alejandro Aruffo  
 6 David Camerini  
 7 Leander Lauffer  
 8 Carmen Oquendo  
 9 David Simmons  
 10 Ivan Stamenkovic  
 11 Siegfried Stengelin  
 12 Martine Amiot  
 15 <120> TITLE OF INVENTION: Rapid Immunoselection Cloning Method  
 17 <130> FILE REFERENCE: 11-88L  
 19 <140> CURRENT APPLICATION NUMBER: US 09/836,544B  
 20 <141> CURRENT FILING DATE: 2001-04-17  
 22 <150> PRIOR APPLICATION NUMBER: US 07/983,647  
 23 <151> PRIOR FILING DATE: 1992-12-01  
 25 <150> PRIOR APPLICATION NUMBER: US 07/553,759  
 26 <151> PRIOR FILING DATE: 1990-07-13  
 28 <150> PRIOR APPLICATION NUMBER: US 07/498,809  
 29 <151> PRIOR FILING DATE: 1990-03-23  
 31 <150> PRIOR APPLICATION NUMBER: US 07/379,076  
 32 <151> PRIOR FILING DATE: 1989-07-13  
 34 <150> PRIOR APPLICATION NUMBER: US 07/160,416  
 35 <151> PRIOR FILING DATE: 1988-02-25  
 37 <160> NUMBER OF SEQ ID NOS: 38  
 39 <170> SOFTWARE: PatentIn Ver. 2.0  
 41 <210> SEQ ID NO: 1  
 42 <211> LENGTH: 2932  
 43 <212> TYPE: DNA  
 44 <213> ORGANISM: Artificial Sequence  
 46 <220> FEATURE:  
 47 <223> OTHER INFORMATION: Description of Artificial Sequence: Nucleotide  
 48 sequence of expression vector, piH3  
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 55 atactgtcct tctagtgtag ccgtagttag gccaccactt caagaactct gtagcaccgc 180  
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 61 cgggggggttc gtgcacacag cccagcttgg agcgaacgac ctacaccgaa ctgagatacc 360  
 63 tacagcgtga gctatgagaa agcgccacgc ttcccgaagg gagaaaggcg gacaggtatc 420  
 65 cggtaaagcg cagggtcgga acaggagagc gcacgaggga gcttcaggcg ggaaacgcct 480  
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73 agggagcagg ccagtaaaag cattaccctgt ggtgggggttc ccgagcggcc aaagggagca 720
75 gactctaaat ctgccgtcat cgacttcgaa ggttcgaatc cttccccccac caccatcact 780
77 ttcaaaagtc cgaaagaatc tgctccctgc ttgtgtgttg gaggtcgtg agtagtgccg 840
79 gagtaaaatt taagctacaa caaggcaagg cttgaccgac aattgcatga agaactctgt 900
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83 attattgact agttattaat agtaatcaat tacgggggtca ttagttcata gcccatatat 1020
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87 ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag ggactttcca 1140
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152 <212> TYPE: DNA
153 <213> ORGANISM: Homo sapiens
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156 <221> NAME/KEY: CDS
157 <222> LOCATION: (7)..(1059)
159 <400> SEQUENCE: 2
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Input Set : A:\11-881.app

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165 Phe Asn Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala
166 15      20      25      30
168 ttg gaa acc tgg ggt gcc ttg ggt cag gac atc aac ttg gac att cct 144
169 Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro
170      35      40      45
173 agt ttt caa atg agt gat gat att gac gat ata aaa tgg gaa aaa act 192
174 Ser Phe Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr
175      50      55      60
177 tca gac aag aaa aag att gca caa ttc aga aaa gag aaa gag act ttc 240
178 Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe
179      65      70      75
181 aag gaa aaa gat aca tat aag cta ttt aaa aat gga act ctg aaa att 288
182 Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile
183      80      85      90
185 aag cat ctg aag acc gat gat cag gat atc tac aag gta tca ata tat 336
186 Lys His Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr
187 95      100      105      110
189 gat aca aaa gga aaa aat gtg ttg gaa aaa ata ttt gat ttg aag att 384
190 Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile
191      115      120      125
193 caa gag agg gtc tca aaa cca aag atc tcc tgg act tgt atc aac aca 432
194 Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr
195      130      135      140
197 acc ctg acc tgt gag gta atg aat gga act gac ccc gaa tta aac ctg 480
198 Thr Leu Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu
199      145      150      155
201 tat caa gat ggg aaa cat cta aaa ctt tct cag agg gtc atc aca cac 528
202 Tyr Gln Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His
203      160      165      170
205 aag tgg acc acc agc ctg agt gca aaa ttc aag tgc aca gca ggg aac 576
206 Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn
207 175      180      185      190
209 aaa gtc agc aag gaa tcc agt gtc gag cct gtc agc tgt cca gag aaa 624
210 Lys Val Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys
211      195      200      205
213 ggt ctg gac atc tat ctc atc att ggc ata tgt gga gga ggc agc ctc 672
214 Gly Leu Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu
215      210      215      220
217 ttg atg gtc ttt gtg gca ctg ctc gtt ttc tat atc acc aaa agg aaa 720
218 Leu Met Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys
219      225      230      235
221 aaa cag agg agt cgg aga aat gat gag gag ctg gag aca aga gcc cac 768
222 Lys Gln Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His
223      240      245      250
225 aga gta gct act gaa gaa agg ggc cgg aag ccc cac caa att cca gct 816
226 Arg Val Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala

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231          275          280          285
233 ggt cat cgt tcc cag gca cct agt cat cgt ccc ccg cct cct gga cac 912
234 Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His
235          290          295          300
237 cgt gtt cag cac cag cct cag aag agg cct cct gct ccg tcg ggc aca 960
238 Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr
239          305          310          315
241 caa gtt cac cag cag aaa ggc ccg ccc ctc ccc aga cct cga gtt cag 1008
242 Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln
243          320          325          330
245 cca aaa cct ccc cat ggg gca gca gaa aac tca ttg tcc cct tcc tct 1056
246 Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser
247 335          340          345          350
249 aat taaaaaagat agaaactgtc tttttcaata aaaagcactg tggatttctg 1109
250 Asn
252 cctcctgat gtgcatatcc gtacttccat gaggtgtttt ctgtgtgcag aacattgtca 1169
254 cctcctgagg ctgtgggcca cagccacctc tgcattctcg aactcagcca tgtggtcaac 1229
256 atctggagtt tttggtctcc tcagagagct ccatcacacc agtaaggaga agcaatataa 1289
258 gtgtgattgc aagaatggta gaggaccgag cacagaaatc ttagagattt cttgtccct 1349
261 ctccaggtcat gtgtagatgc gataaatcaa gtgattggtg tgccctgggtc tctactacaag 1409
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269 <211> LENGTH: 351
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278 20 25 30
280 Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
281 35 40 45
283 Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
284 50 55 60
286 Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
287 65 70 75 80
289 Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
290 85 90 95
292 Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
293 100 105 110
295 Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
296 115 120 125
298 Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
299 130 135 140
301 Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln

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304 Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
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307 Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
308          180          185          190
310 Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
311          195          200          205
313 Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met
314          210          215          220
316 Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln
317 225          230          235          240
319 Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
320          245          250          255
322 Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr
323          260          265          270
325 Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Gly His
326          275          280          285
328 Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
329          290          295          300
331 Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
332 305          310          315          320
334 His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys
335          325          330          335
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355 ctc agc gtg gtc tgc ctg ctg cac tgc ttt ggt ttc atc agc tgt ttt 99
356 Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe
357          15          20          25
359 tcc caa caa ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta 147
360 Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val
361 30          35          40          45
363 cca agc aat gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat 195
364 Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp
365          50          55          60
367 aaa gtt gca gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt 243
368 Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe
369          65          70          75
371 aaa aat agg gtt tat tta gac act gtg tca ggt agc ctc act atc tac 291

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Input Set : A:\11-881.app  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:38; Xaa Pos. 1,4

**VERIFICATION SUMMARY**

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Output Set: **N:\CRF4\01262005\I836544B.raw**

L:3496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0